RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/575,192 _____
Source: _____ IFWP _____
Date Processed by STIC: _____ 04/24/2006 _____

ENTERED

IFWP

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          RAW SEQUENCE LISTING              DATE: 04/24/2006
          PATENT APPLICATION:  US/10/575,192   TIME: 16:12:56

          Input Set : A:\14875-159US1.txt
          Output Set: N:\CRF4\04242006\J575192.raw

    3 <110> APPLICANT: Igawa, Tomoyuki
    4         Sekimori, Yasuo
    6 <120> TITLE OF INVENTION: IgM high concentration stabilized solution
    8 <130> FILE REFERENCE: 14875-159US1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,192
C--> 10 <141> CURRENT FILING DATE: 2006-04-07
   10 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/14935
   11 <151> PRIOR FILING DATE: 2004-10-08
   13 <150> PRIOR APPLICATION NUMBER: JP 2003-351388
   14 <151> PRIOR FILING DATE: 2003-10-09
   16 <160> NUMBER OF SEQ ID NOS: 18
   18 <170> SOFTWARE: PatentIn version 3.1
   20 <210> SEQ ID NO: 1
   21 <211> LENGTH: 1779
   22 <212> TYPE: DNA
   23 <213> ORGANISM: Homo sapiens
   25 <220> FEATURE:
   26 <221> NAME/KEY: CDS
   27 <222> LOCATION: (1)..(1779)
   28 <223> OTHER INFORMATION:
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   32 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
   33 1               5                   10                  15
   35 gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag    96
   36 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
   37             20                  25                  30
   39 cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt   144
   40 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
   41         35                  40                  45
   43 agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg   192
   44 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
   45     50                  55                  60
   47 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca   240
   48 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
   49 65                  70                  75                  80
   51 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac   288
   52 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
   53                 85                  90                  95
   55 acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta   336
   56 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
   57                100                 105                 110
   59 tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct   384
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 60 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
 61         115                 120                 125
 63 tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc        432
 64 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
 65         130                 135                 140
 67 cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg        480
 68 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
 69 145                 150                 155                 160
 71 agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc        528
 72 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
 73         165                 170                 175
 75 atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc        576
 76 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
 77         180                 185                 190
 79 cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca        624
 80 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
 81         195                 200                 205
 83 cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac        672
 84 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
 85         210                 215                 220
 87 gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg        720
 88 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
 89 225                 230                 235                 240
 91 cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc        768
 92 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
 93                 245                 250                 255
 95 cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc        816
 96 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
 97                 260                 265                 270
 99 tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg        864
100 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
101             275                 280                 285
103 cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag        912
104 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
105         290                 295                 300
107 gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca        960
108 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
109 305                 310                 315                 320
111 ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc       1008
112 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
113             325                 330                 335
115 cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg       1056
116 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
117         340                 345                 350
119 tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca       1104
120 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
121         355                 360                 365
123 tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg       1152
124 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
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125     370                   375                  380
127 gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc     1200
128 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
129 385                   390                  395                  400
131 cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac     1248
132 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
133                   405                  410                  415
135 ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat     1296
136 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
137                   420                  425                  430
139 gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac     1344
140 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
141             435                  440                  445
143 ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc     1392
144 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
145         450                  455                  460
147 ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg     1440
148 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
149 465                   470                  475                  480
151 aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct     1488
152 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
153                   485                  490                  495
155 ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc     1536
156 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
157         500                  505                  510
159 ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca     1584
160 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
161         515                  520                  525
163 ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg     1632
164 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
165     530                  535                  540
167 aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc     1680
168 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
169 545                   550                  555                  560
171 aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc     1728
172 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
173             565                  570                  575
175 ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac     1776
176 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
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179 tga                                                                 1779
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 592
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
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189 1           5                   10                  15
190 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
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RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,192   TIME: 16:12:56

Input Set : A:\14875-159US1.txt
Output Set: N:\CRF4\04242006\J575192.raw

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191          20                25                30
192 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
193          35                40                45
194 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
195          50                55                60
196 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
197 65                70                75                80
198 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
199                85                90                95
200 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
201          100               105               110
202 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
203          115               120               125
204 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
205          130               135               140
206 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
207 145               150               155               160
208 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
209                165               170               175
210 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
211          180               185               190
212 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
213          195               200               205
214 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
215          210               215               220
216 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
217 225               230               235               240
218 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
219                245               250               255
220 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
221          260               265               270
222 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
223          275               280               285
224 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
225          290               295               300
226 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
227 305               310               315               320
228 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
229                325               330               335
230 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
231          340               345               350
232 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
233          355               360               365
234 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
235          370               375               380
236 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
237 385               390               395               400
238 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
239                405               410               415
```

```
240 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
241         420                 425                 430
242 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
243         435                 440                 445
244 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
245         450                 455                 460
246 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
247 465                 470                 475                 480
248 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
249         485                 490                 495
250 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
251         500                 505                 510
252 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
253         515                 520                 525
254 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
255         530                 535                 540
256 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
257 545                 550                 555                 560
258 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
259         565                 570                 575
260 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
261         580                 585                 590
264 <210> SEQ ID NO: 3
265 <211> LENGTH: 723
266 <212> TYPE: DNA
267 <213> ORGANISM: Homo sapiens
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (1)..(723)
272 <223> OTHER INFORMATION:
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275 atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct      48
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277 1               5                   10                  15
279 ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct      96
280 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
281             20                  25                  30
283 gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt     144
284 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
285         35                  40                  45
287 gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag     192
288 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
289         50                  55                  60
291 aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg     240
292 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
293 65                  70                  75                  80
295 gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat     288
296 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
297             85                  90                  95
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/24/2006
PATENT APPLICATION: **US/10/575,192**   TIME: 16:12:57

Input Set : **A:\14875-159US1.txt**
Output Set: **N:\CRF4\04242006\J575192.raw**

<u>**Invalid <213> Response:**</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY   DATE: 04/24/2006
PATENT APPLICATION: **US/10/575,192**   TIME: 16:12:57

Input Set : **A:\14875-159US1.txt**
Output Set: **N:\CRF4\04242006\J575192.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:274 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:272
L:386 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:384